

FEATURES:

5'UTR: 1-227 Start Codon: 228 Stop Codon: 2073 3'UTR: 2076

Homologous proteins:

Top 10 BLAST Hits		
	Score	E
CRA 1000682340958 /altid=gi 6358505 /def=gb AAF07219.1 AF043722	1293	0.0
CRA 18000005086608 /altid=gi 5031623 /def=ref NP_005816.1 RAS	1241	0.0
CRA 18000005188697 /altid=gi 6755290 /def=ref NP_035372.1 RAS,	1202	0.0
CRA 18000005205935 /altid=gi 7662334 /def=ref NP_056191.1 KIAA	618	e-175
CRA 18000005188699 /altid=gi 3928857 /def=gb AAC79700.1 (AF081	533	e-150
CRA 18000005152782 /altid=gi 9507035 /def=ref NP_062084.1 RAS	531	e-149
CRA 18000005192860 /altid=qi 7242201 /def=ref NP 035376.1 RAS	529	e-149
CRA 18000005192861 /altid=qi 4038292 /def=gb AAC97349.1 (AF106	526	e-148
CRA 18000005188698 /altid=qi 5032025 /def=ref NP 005730.1 RAS	525	e-148
CRA 1000733831533 /altid=gi 6650545 /def=gb AAF21898.1 AF081197	525	e-148
BLAST dbEST hits:		
	Score	E
gi 5432583 /dataset=dbest /taxon=9606	1310	0.0
gi 9876673 /dataset=dbest /taxon=960	1281	0.0
gi 11286864 /dataset=dbest /taxon=96	1249	0.0
gi 11285315 /dataset=dbest /taxon=96	1207	0.0
gi 5432584 /dataset=dbest /taxon=9606	733	0.0
gi 4372300 /dataset=dbest /taxon=9606	720	0.0
gi 12295751 /dataset=dbest /taxon=96	700	0.0
gi 12288965 /dataset=dbest /taxon=96	599	e-168
gi 6920402 /dataset=dbest /taxon=960	573	e-161
gi 2005039 /dataset=dbest /taxon=9606	573	e-161
EXPRESSION INFORMATION FOR MODULATORY USE:		
library source:		
From BLAST dbEST hits:		
gi 5432583 Testis		
gi 9876673 Liver-non-cancerous		
gi 11286864 Brain glioblastoma		
gi 11285315 Brain glioblastoma		
gi 5432584 Testis		
gi 4372300 B Cell Chronic lymphatic leukemia		
gi 12295751 Adult marrow		
gi 12288965 Adult marrow		
gi 6920402 Lymph germinal center B cell		
gi 2005039 Lymph		

From tissue screening panels: Leukocyte

```
1 MAGTLDLDKG CTVEELLRGC IEAFDDSGKV RDPQLVRIFL MMHPWYIPSS
  51 QLAAKLLHIY QQSRKDNSNS LQVKTCHLVR YWISAFPAEF DLNPELAEQI
 101 KELKALLDQE GNRRHSSLID IDSVPTYKWK RQVTQRNPVG QKKRKMSLLF
 151 DHLEPMELAE HLTYLEYRSF CKILFQDYHS FVTHGCTVDN PVLERFISLF
 201 NSVSQWVQLM ILSKPTAPQR ALVITHFVHV AEKLLQLQNF NTLMAVVGGL
 251 SHSSISRLKE THSHVSPETI KLWEGLTELV TATGNYGNYR RRLAACVGFR
 301 FPILGVHLKD LVALQLALPD WLDPARTRLN GAKMKQLFSI LEELAMVTSL
 351 RPPVQANPDL LSLLTVSLDQ YQTEDELYQL SLQREPRSKS SPTSPTSCTP
  401 PPRPPVLEEW TSAAKPKLDQ ALVVEHIEKM VESVFRNFDV DGDGHISQEE
  451 FQIIRGNFPY LSAFGDLDQN QDGCISREEM VSYFLRSSSV LGGRMGFVHN
  501 FQESNSLRPV ACRHCKALIL GIYKQGLKCR ACGVNCHKQC KDRLSVECRR
  551 RAQSVSLEGS APSPSPMHSH HHRAFSFSLP RPGRRGSRPP AIPLPAEIRE
  601 EEVOTVEDGV FDIHL (SEQ ID NO:2)
FEATURES:
Functional domains and key regions:
[1] PDOC00004 PS00004 CAMP PHOSPHO SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site
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```
Number of matches: 3
           113-116 RRHS
      1
      2
           144-147 RKMS
           584-587 RRGS
```

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site

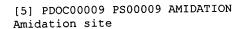
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Number of matches: 7
             27-29 SGK
      1
             63-65 SRK
           126-128 TYK
           134-136 TQR
      4
           269-271 TIK
      5
      6
           349-351 SLR
           506-508 SLR
```

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site

```
Number of matches: 9
             12-15 TVEE
      1
             63-66 SRKD
           117-120 SLID
      3
           163-166 TYLE
      4
      5
           339-342 SILE
           373-376 TEDE
      6
      7
           447-450 SQEE
           476-479 SREE
      8
           605-608 TVED
      9
```

[4] PDOC00008 PS00008 MYRISTYL N-myristoylation site

```
Number of matches: 4
           19-24 GCIEAF
      1
           249-254 GLSHSS
      2
           284-289 GNYGNY
      3
           492-497 GGRMGF
```



582-585 PGRR

[6] PDOC00018 PS00018 EF_HAND EF-hand calcium-binding domain

Number of matches: 2

- 1 439-451 DVDGDGHISQEEF
- 2 468-480 DQNQDGCISREEM

[7] PDOC00379 PS00479 DAG_PE_BIND_DOM_1 Phorbol esters / diacylglycerol binding domain

499-548 HNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQCKDRLSVEC

Membrane spanning structure and domains:

Helix		End	Score	Certainty
1	34	54	0.713	Putative
2	195	215	0.653	Putative
3	238	258	0.788	Putative

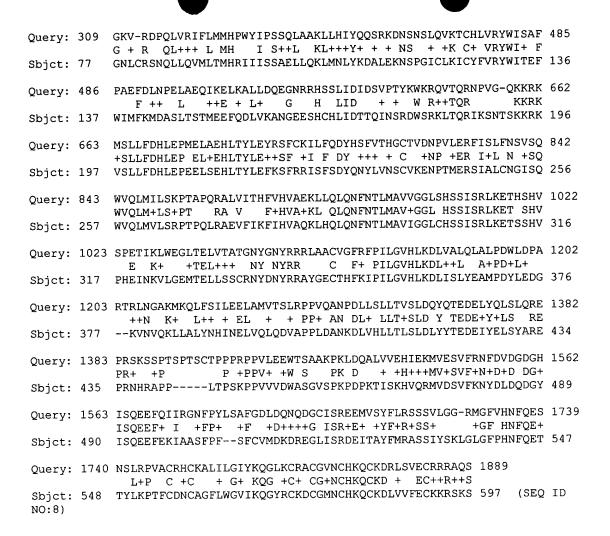
BLAST Alignment to Top Hit:

>CRA|18000005086608 /altid=gi|5031623 /def=ref|NP 005816.1| RAS guanyl releasing protein 2 (calcium and DAG-regulated); calcium and diacylglycerol-regulated guanine nucleotide exchange factor I [Homo sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa /length=609 Length = 609Score = 1241 bits (3176), Expect = 0.0Identities = 608/615 (98%), Positives = 609/615 (98%) Frame = +3Query: 228 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 407 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVR+FLMMHPWYIPSSQLAAKLLHIY MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLAAKLLHIY 60 Sbjct: 1 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 587 Query: 408 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 120 Sbjct: 61 Query: 588 IDSVPTYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 767 IDSVPTYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS Sbjct: 121 IDSVPTYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180 Query: 768 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 947 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF Sbjct: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 240 Query: 948 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR 1127 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR Sbjct: 241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR 300 Query: 1128 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 1307 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL Sbjct: 301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 360 Query: 1308 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 1487 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ Sbjct: 361 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420 Query: 1488 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 1667 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM Sbjct: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 480 Query: 1668 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 1847 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540 Query: 1848 KDRLSVECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPPAIPLPAEIRE 2027 KDRLSVECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP Sbjct: 541 KDRLSVECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP----EIRE 594 Query: 2028 EEVQTVEDGVFDIHL 2072 EEVQTVEDGVFDIHL Sbjct: 595 EEVQTVEDGVFDIHL 609 (SEQ ID NO:4)

```
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           sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa
           /length=671
         Length = 671
Score = 1293 bits (3309), Expect = 0.0
Identities = 639/670 (95%), Positives = 643/670 (95%), Gaps = 4/670 (0%)
Frame = +3
           GRGGVKLPQGPPRAGREGAPGGGGAAG----GVRSEPGGRLPERSLGPAHPAPAAMAGTL 242
Query: 75
                                           GVRSEPGGRLPERSLGPAHPAPAAMAGTL
                  Р
                                  G +G
            GRGTQGWPGSSEQHVQEATSSAGLHSGVDELGVRSEPGGRLPERSLGPAHPAPAAMAGTL 67
Sbict: 8
           DLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIYQQSRK 422
Query: 243
            DLDKGCTVEELLRGCIEAFDDSGKVRDPQLVR+FLMMHPWYIPSSQLAAKLLHIYQQSRK
            DLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLAAKLLHIYQQSRK 127
Sbjct: 68
           DNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLIDIDSVP 602
Query: 423
            DNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLIDIDSVP
            DNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLIDIDSVP 187
Sbict: 128
           TYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHSFVTHG 782
Query: 603
            TYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHSFVTHG
           TYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHSFVTHG 247
Sbjct: 188
Query: 783 CTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNFNTLMA 962
            CTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNFNTLMA
Sbjct: 248 CTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNFNTLMA 307
Query: 963 VVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFRFPILG 1142
            VVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFRFPILG
Sbjct: 308 VVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFRFPILG 367
Query: 1143 VHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDLLSLLT 1322
            VHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDLLSLLT
           VHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDLLSLLT 427
Sbict: 368
Query: 1323 VSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQALVVE 1502
            VSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQALVVE
            VSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQALVVE 487
Sbjct: 428
Query: 1503 HIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEMVSYFL 1682
            HIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEMVSYFL
Sbjct: 488 HIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEMVSYFL 547
Query: 1683 RSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQCKDRLS 1862
            RSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQCKDRLS
Sbjct: 548 RSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQCKDRLS 607
Query: 1863 VECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPPAIPLPAEIREEEVQT 2042
                                                               EIREEEVQT
            VECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP
Sbjct: 608 VECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP-----EIREEEVQT 661
Query: 2043 VEDGVFDIHL 2072
            VEDGVFDIHL
Sbjct: 662 VEDGVFDIHL 671 (SEQ ID NO:5)
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>CRA|18000005188697 /altid=gi|6755290 /def=ref|NP_035372.1| RAS,
            guanyl releasing protein 2; RAP 1A protein-specific
            quanine nucleotide exchange factor 1; CalDAG-GEFI [Mus
            musculus] /org=Mus musculus /taxon=10090 /dataset=nraa
            /length=608
          Length = 608
 Score = 1202 \text{ bits } (3076), \text{ Expect = } 0.0
 Identities = 589/615 (95%), Positives = 597/615 (96%)
 Frame = +3
Query: 228 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 407
            MA TLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVR+FLMMHPWYIPSSQLA+KLLH Y
            MASTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLASKLLHFY 60
Sbjct: 1
            QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 587
Query: 408
            QQSRKDNSNSLQVKTCHLVRYW+SAFPAEFDLNPELAE IKELKALLDQEGNRRHSSLID
Sbjct: 61
            QQSRKDNSNSLQVKTCHLVRYWVSAFPAEFDLNPELAEPIKELKALLDQEGNRRHSSLID 120
Query: 588 IDSVPTYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 767
            I+SVPTYKWKRQVTQRNPV QKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS
Sbjct: 121 IESVPTYKWKRQVTQRNPVEQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180
Query: 768 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNF 947
            FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTA QRALVITHFVHVAEKLLQLQNF
Sbjct: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTATQRALVITHFVHVAEKLLQLQNF 240
Query: 948 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFR 1127
            NTLMAVVGGLSHSSISRLKETHSHVSP+TIKLWEGLTELVTATGNY NYRRRLAACVGFR
Sbjct: 241 NTLMAVVGGLSHSSISRLKETHSHVSPDTIKLWEGLTELVTATGNYSNYRRRLAACVGFR 300
Query: 1128 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 1307
            FPILGVHLKDLVALQLALPDWLDP RTRLNGAKM+QLFSILEELAMVTSLRPPVQANPDL
Sbjct: 301 FPILGVHLKDLVALQLALPDWLDPGRTRLNGAKMRQLFSILEELAMVTSLRPPVQANPDL 360
Query: 1308 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 1487
            LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTS AKPKLDQ
Sbjct: 361 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSVAKPKLDQ 420
Query: 1488 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 1667
            ALV EHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM
Sbjct: 421 ALVAEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 480
Query: 1668 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 1847
            +SYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC
Sbjct: 481 ISYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540
Query: 1848 KDRLSVECRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPPAIPLPAEIRE 2027
            KDRLSVECRRRAQSVSLEGSAPSPSP H+ HHRAFSFSLPRPGRR SRPP
Sbjct: 541 KDRLSVECRRRAQSVSLEGSAPSPSPTHT-HHRAFSFSLPRPGRRSSRPP-----EIRE 593
Query: 2028 EEVQTVEDGVFDIHL 2072
            EEVQTVEDGVFDIHL
Sbjct: 594 EEVQTVEDGVFDIHL 608 (SEQ ID NO:6)
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```
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           protein [Homo sapiens] /org=Homo sapiens /taxon=9606
           /dataset=nraa /length=689
         Length = 689
 Score = 618 \text{ bits } (1576), \text{ Expect} = e-175
 Identities = 314/597 (52%), Positives = 409/597 (67%), Gaps = 5/597 (0%)
 Frame = +3
Query: 234 GTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIYQQ 413
           G+ L K T++ELL CIE FDD+G++ + L RI L+MH WY+ S++LA KLL +Y+
           GSSGLGKAATLDELLCTCIEMFDDNGELDNSYLPRIVLLMHRWYLSSTELAEKLLCMYRN 61
Sbjct: 2
           SRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLIDID 593
Query: 414
            + ++ N ++K C+ +RYWI FPAEF+L+ L
                                                 +E + + Q G +H SLIDI
           ATGESCNEFRLKICYFMRYWILKFPAEFNLDLGLIRMTEEFREVASQLGYEKHVSLIDIS 121
Sbjct: 62
           SVPTYKWKRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHSFV 773
Query: 594
            S+P+Y W R+VTQR V KK K LLFDHLEP+ELAEHLT+LE++SF +I F DY S+V
Sbjct: 122 SIPSYDWMRRVTQRKKVS-KKGKACLLFDHLEPIELAEHLTFLEHKSFRRISFTDYQSYV 180
Query: 774 THGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLLQLQNFNT 953
            HGC +NP LER I+LFN +S+WVQLM+LSKPT QRA VIT F++VA+KLLQL+NFNT
Sbjct: 181 IHGCLENNPTLERSIALFNGISKWVQLMVLSKPTPQQRAEVITKFINVAKKLLQLKNFNT 240
Query: 954 LMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNYRRRLAACVGFRFP 1133
            LMAVVGGLSHSSISRLKETHSH+S E K W +TELV++ GNY NYR+ A C GF+ P
Sbjct: 241 LMAVVGGLSHSSISRLKETHSHLSSEVTKNWNEMTELVSSNGNYCNYRKAFADCDGFKIP 300
Query: 1134 ILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDLLS 1313
            ILGVHLKDL+A+ + PDW + ++N KM QL L EL + +
                                                              ++ N DL++
Sbjct: 301 ILGVHLKDLIAVHVIFPDWTE--ENKVNIVKMHQLSVTLSELVSLQNASHHLEPNMDLIN 358
Query: 1314 LLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQAL 1493
            LLT+SLD Y TED++Y+LSL EPR+ SPTSPT+ P +P V EW
Sbjct: 359 LLTLSLDLYHTEDDIYKLSLVLEPRNSKSPTSPTT---PNKPVVPLEWALGVMPKPDPTV 415
Query: 1494 VVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEMVS 1673
            + +HI K+VESVFRN+D D DG+ISQE+F+ I NFP+L +F LD++QDG IS++EM++
Sbjct: 416 INKHIRKLVESVFRNYDHDHDGYISQEDFESIAANFPFLDSFCVLDKDQDGLISKDEMMA 475
Query: 1674 YFLRSSSVLGGRM--GFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 1847
            YFLR+ S L +M GF+HNFQE L+P C HC + GI KQG KC+ CG NCHKQC
Sbjct: 476 YFLRAKSQLHCKMGPGFIHNFQEMTYLKPTFCEHCAGFLWGIIKQGYKCKDCGANCHKQC 535
Query: 1848 KDRLSVECRRRAQSVSL---EGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPPAIPL 2009
                                                FF
                                                        GR
                                                                AT L
            KD L + CRR A++ SL
                              GS P
Sbjct: 536 KDLLVLACRRFARAPSLSSGHGSLPGSPSLPPAQDEVFEFPGVTAGHRDLDSRAITL 592 (SEQ
ID NO:7)
>CRA|18000005188699 /altid=gi|3928857 /def=gb|AAC79700.1| (AF081196)
            calcium and DAG-regulated guanine nucleotide exchange
            factor II [Rattus norvegicus] /org=Rattus norvegicus
            /taxon=10116 /dataset=nraa /length=795
          Length = 795
 Score = 533 \text{ bits } (1358), Expect = e-150
 Identities = 267/590 (45%), Positives = 390/590 (65%), Gaps = 12/590 (2%)
 Frame = +3
Query: 156 GVRSEPGGRLPERSLGPAHPAPAAMAGTLD-----LDKGCTVEELLRGCIEAFDDS 308
                                                   L KG ++++L+ CI++FD
            G R+ P GRL +S
                              PA ++A
            GSRAGPKGRLEAKSTNSPLPAQPSLAQITQFRMMVSLGHLAKGASLDDLIDSCIQSFDAD 76
Sbjct: 17
```



Hmmer search results (Pfam):

Model	Description	Score	E-value	<u>N</u>
PF00617	RasGEF domain	123.5	4e-33	1
PF00130	Phorbol esters/diacylglycerol binding domain	59.5	3.6e-14	1
	EF hand	21.8	0.00027	2
PF01237	Oxysterol-binding protein	3.5	4.2	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t		score	E-value
PF01237	1/1	249	272	 1	24	[.	3.5	4.2
PF00617	1/1	148	336	 1	227	[]	123.5	4e-33
PF00036	1/2	430	458	 1	29	[]	17.4	0.0047
PF00036	2/2	463	482	 5	24		6.7	4.9
PF00130	1/1	499	548	 1	51	f 1	59.5	3.6e-14

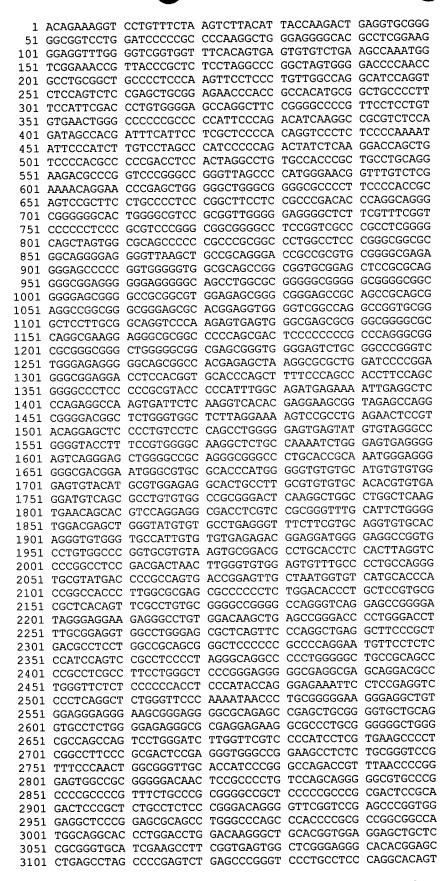


FIGURE 3, page 1 of 12

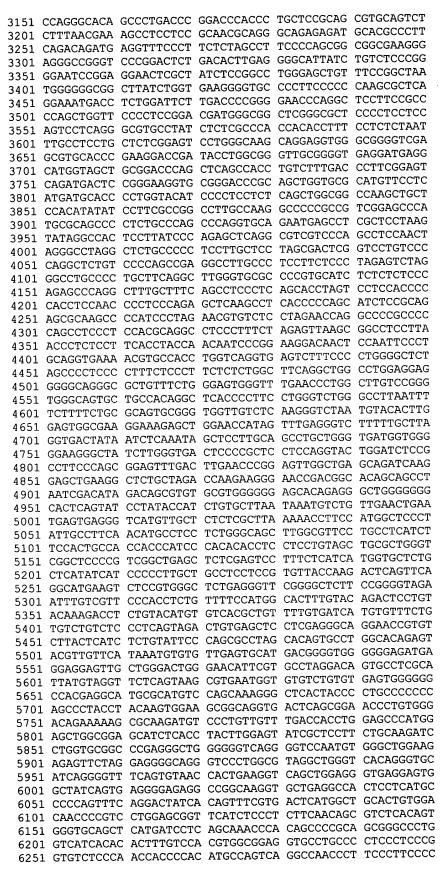
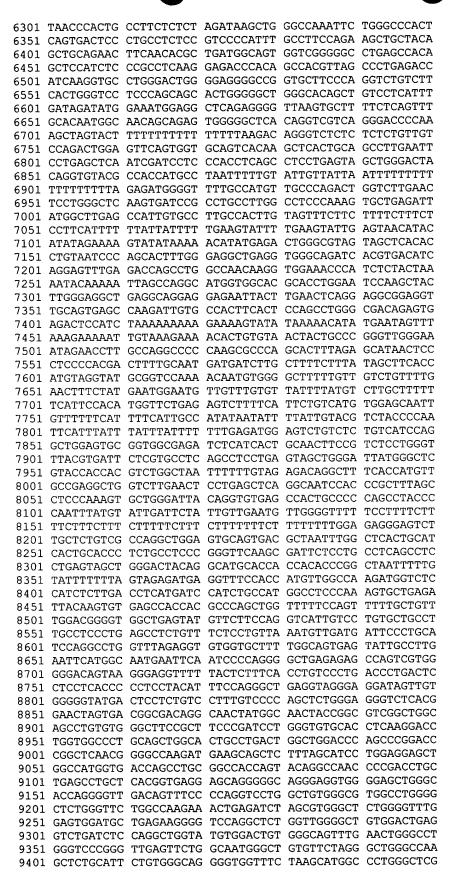


FIGURE 3, page 2 of 12



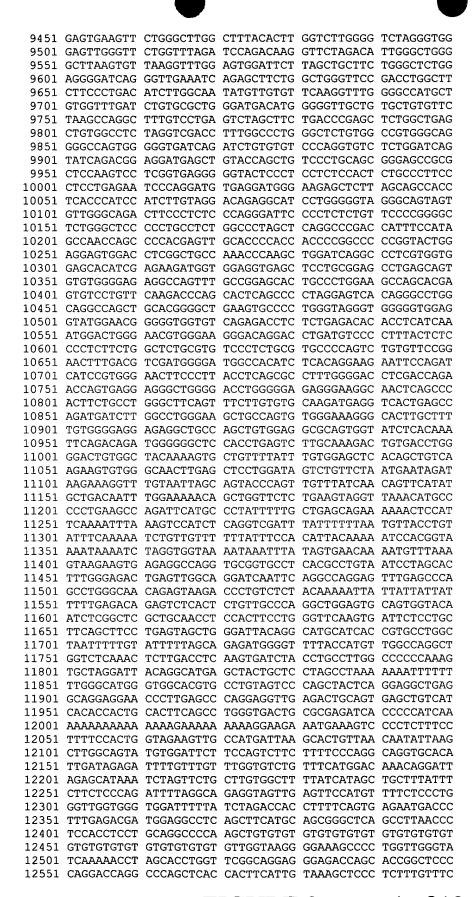
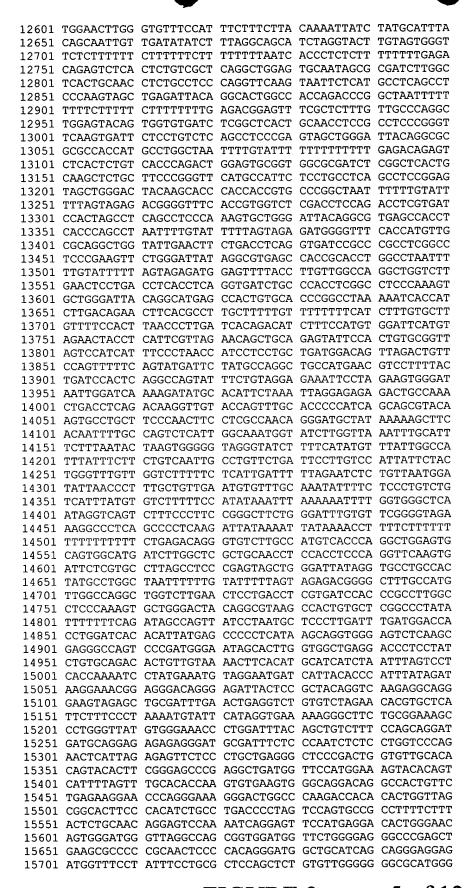
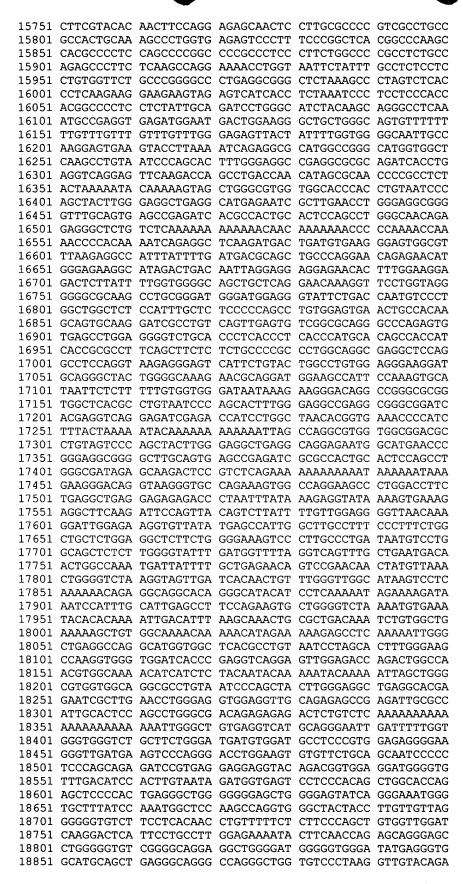


FIGURE 3, page 4 of 12





18901 CTCTTGTGAA TATTTGTATT TTCCAGATGG AATAAAAAGG CCCGTGTAAT 18951 TAACCTTCAC CATCAGCGCC TAGAATCCCG GGGGGTAGGG GGATGGTATA 19001 CTTTACAGGA TGACAATCTT GGGAGCTAGA ACTTTGTAGC CAGAGAAACT 19051 TGGGAGGTCT GGAATCTCAT GTGTCTGGAG TCTTGGGGAA GAGAATCTTA 19101 GAAGCAGAAA ACCTTGGAAC ATAAGAATCT TGGGGAGGGT CTAGGATCTT 19151 GAGGAGACCA GATCCTTGGA CATCTAAAAC TTGAAACTAG TAGGTCTGCA 19201 CCCGAGAATT GCAGGGCCAG TCATGCATAC CCAAAGCCTT CAGCCCATGG 19251 CCGAAATTCC CTTGCTGGAC AGGGGGCCTT TCAGCCCCTG CTTGGACGCT 19301 TCCAGTAACA GGGCCCTCAC TGCAGGAATC GTGGGAGGGA GAGGGGCAGC 19351 ACAGAGTTGC TGGCTGTCGG GGAAGGGAGG GAGGGCCCTG GGCAGTCCGA 19401 GGGCCCTGCT GGGCTTGTGC CTCAGGGTGG GGGCTGCACT CCTCCGCCTT 19451 GCAGCCTCCT GGCCTGGTGC TGCTGCCAGC CGGAAGGACA GTGACTTCCA 19501 GAGGAAATGC ATATTGATCC TGCTTTCAGC CTCCGGTGGT GGCTTCTCCC 19551 AACCCAGCTC TTCCCTCCTG AGCCTGCAGC ACGGAGGTTT TGGGGGTCAC 19601 TGCTACCTAA AGAAGGCTAA GGCCACTTCT GAGGCTGGTC TGGGAGTTTA 19651 CTAAAGGTTC TGAAGCTGGG CCGGGCTGCC CCTGGGATCA GGAGACTCCA 19701 GACAGCAGTC CTGACAATGG GAACTACCTC CTCAGTCCCC CAAACTGGGA 19751 GGTGTCCCAC AGCAGCTGTA GGATTGTCCT AGGGGTGGAG ACCTGAGCAC 19801 CTTCCACTCC AAAGCACAGT ATCTGTGGGC CTGGCAGTGG CCTCAGTTCC 19851 CCCATGAGTG CCCCGGTCCC CCACCCCAGG GTTTCCCCAC ATCACATCCA 19901 TCCCTGCTTT GAGACCCCAC TCCCCCTGGC CTGTTCTTTA TTTTGGGTCA 19951 CTCCCTTCTC TTTCCTGGTC ATATCTCTCC TGCAGGCCTA CCCTGTGTTG 20001 GGCCCCCAG CCCTGTCTCT GCATCGGGTG CCCCCCTGCC CCTCCTTCTG 20051 TCCTCAGCCC CCTCCGCCCT TCCCCCTCTT GAGGCTGTAA TATCCGTTTC 20101 ACGATTTGGG GGCTGAGTTG CTATAACAAC AGACGGCGAT TGTGTTGTGA 20151 AGAGCAGCTC GCTCCTGTGC CGCCTGCCTC CTGTGCTGCC TCCATCCCTG 20201 CAGCCCAGTC GGTTCCTCTT GGCTCCTCTC GTCACTACCC TCCAGTTCCA 20301 GCATGCATGC ATATGTGTGT CCAGGTCTGC CTGCCCGGGA TGTGACAAGT 20351 AGCGGTCTTC ATGGTTGCAT GTGTCTGAAT TTGGTGTCTG AGCTTCACAT 20401 TGTATGCGCC TGTGTGCATG TGTGTGCATG GACATGCATG CTGTATCTGC 20451 TGTGTTTCCC CTCCCCCATG TGTCCCCACT GGCCTTTGCA CATGGGAGAA 20501 GGGCATGTGC TCAGCATATC ACTCAACTGT CCACATTGGG TGGGTACCTG 20551 TGTGTGGTGT GTGTGTGGG GGGGTGTGTC TTGAAGTGGC AGGTCCCAAA 20601 TGCTTAGGCA ATCTGAACCT TGGACCTTGC AGAGAGGAGA GATGTCCCTG 20651 TAGGTGGGAG GGACAGGGAG ATGCAGCAGC TGCCCGGTGA CCTTTTCTGC 20701 CCTTGATGGG CAAAGCTGGG GGTAGGGAAA GGAGACAAGT GCTCATACTT 20751 ACCTCCCTCC CTGCCCAGGC TCCTCTGTAA GGGTCTGAGT CTGTCTCTGT 20801 GAGCCATTGC ATCTGTCTGT CTATGCCCTG ATGCCTGGAT GGACAAGGGG 20851 TGTGTGTGTG TGTGTGTGT TGTGTGTGTG AGTGTGAGGC TGCAGGAAGA 20901 GGAACAGTGG GGGATGGGCA GGAAAGTGGG CTGTGGGGTC AGGGAGGCGA 20951 T (SEO ID NO:3)

FEATURES:

3000 Start: Exon: 3000-3072 3073-3753 Intron: 3754-3855 Exon: Intron: 3856-4363 4364-4427 Exon: 4428-4786 Intron: 4787-4918 Exon: 4919-5702 Intron: Exon: 5703-5853 5854-6056 Intron: Exon: 6057-6230 6231-6389 Intron: 6390-6506 Exon: Intron: 6507-8832 8833-9114 Exon: 9115-9885 Intron: Exon: 9886-9963 Intron: 9964-10201 Exon: 10202-10324 Intron: 10325-10638 10639-10754 Exon: Intron: 10755-15675 Exon: 15676-15817 15818-16071 Intron: Exon: 16072-16108 Intron: 16109-16828 16829-17008 Exon: Intron: 17009-18491 18492-18565 Exon: Stop: 18566

CHROMOSOME MAP POSITION:

Chromosome 11

ALLELIC VARIANTS (SNPs):

DNA

Position	Major	Minor	Domain
5539	С	G	Intron
5658	T	G	Intron
5861	С	T	Intron
6023	A	G	Intron
6799	С	T	Intron
9579	С	A	Intron
9842	T	C	Intron
10159	T	С	Intron
12025	A	- G	Intron
14723	T	С	Intron
14996	G	A	Intron
16153	T	G	Intron
16181	G	A	Intron
16756	A	G	Intron
18059	A	G	Intron
18364	A	- T	Intron
18861	G	A	Beyond ORF(3')
20443	G	A	Beyond ORF(3')
20881	A	T	Beyond ORF(3')

Context:

DNA Position

5539

5658

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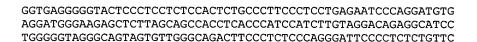
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CTCACTACCCCTGCCCCCCAGCCCTACCTACAAGTGGAAGCGCAGGTGACTCAGCGGA
ACCCTGTGGGACAGAAAAAGCGCAAGATGTCCCTGTTGTTTGACCACCTGGAGCCCATGG
AGCTGGCGGAGCATCTCACCTACTTGGAGTATCGCTCCTTCTGCAAGATCCTGGTGCGGC
[C,T]

CGAGGGCTGGGGGGTCAGGGGTCCAATGTGGGCTGGAAGAGAGTTCTAGGAGGGGCAGGG TCCCTGGCGTAGGCTGGGTCACAGGGTGCATCAGGGGTTTCAGTGTAACCACTGAAGGTC AGCTGGAGGGTGAGGAGTGGCTATCAGTGAGGGGAGAGGCCGGCAAGGTGCTGAGGCCAC TCCTCATGCCCCCAGTTTCAGGACTATCACAGTTTCGTGACTCATGGCTGCACTGTGGAC AACCCCGTCCTGGAGCGGTTCATCTCCCTCTTCAACAGCGTCTCACAGTGGGTGCAGCTC

GGCAGGTGACTCAGCGGAACCCTGTGGGACAGAAAAAGCGCAAGATGTCCCTGTTGTTTG
ACCACCTGGAGCCCATGGAGCTGGCGGAGCATCTCACCTACTTGGAGTATCGCTCCTTCT
GCAAGATCCTGGTGCGGCCCGAGGGCTGGGGGGTCAGGGGTCCAATGTGGGCTGGAAGAG
AGTTCTAGGAGGGGCAGGGTCCCTGGCGTAGGCTGGGTCACAGGGTGCATCAGGGGTTTC
AGTGTAACCACTGAAGGTCAGCTGGAGGGTGAGGAGTGCTATCAGTGAGGGGAGAGGCC
[A.G]

GTGGGCAGGGGCCAGTGGGGGTGATCAGATCTGTGTGTCCCAGGTGTCTCTGGATCAGTA
TCAGACGGAGGATGAGCTGTACCAGCTGTCCCTGCAGCGGGAGCCGCGCTCCAAGTCCTC

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GGGGGTGATCAGATCTGTGTCCCAGGTGTCTCTGGATCAGTATCAGACGGAGGATGAG
CTGTACCAGCTGTCCCTGCAGCGGGAGCCGCGCTCCAAGTCCTCGGTGAGGGGGTACTCC
CTCCTCTCCACTCTGCCCTTCCCTCTGAGAATCCCAGGATGTGAGGATGGGAAGAGCTC
TTAGCAGCCACCTCACCCATCCATCTTGTAGGACAGAGGCATCCTGGGGGTAGGGCAGTA
GTGTTGGGCAGACTTCCCTCCCCAGGGATTCCCCTCTCTGTTCCCCGGGGCTCTGGGCT

[T.C]

CCCCTGCCTCTGGCCCTAGCTCAGGCCCGACCATTTCCATAGCCAACCAGCCCCACGAGT
TGCACCCCACCACCCCGGCCCCCGGTACTGGAGGAGTGGACCTCGGCTGCCAAACCCAAG
CTGGATCAGGCCCTCGTGGTGGAGCACATCGAGAAGATGGTGGAGGTGAGCTCCTGCGGA
GCCTGAGCAGTGTGTGGGGGAGAGGCCAGTTTGCCGGAGCACTGCCCTGGAAGCCAGCACC
AGTGTCCTGTTCAAGACCCAGCACTCAGCCCCTAGGAGTCACAGGGCCTGGCAGGCCAGC

> CTGACCTCGTGATCCACCCGCCTTGGCCTCCCAAAGTGCTGGGACTACAGGCGTAAGCCA CTGTGCTCGGCCCTATATTTTTTTCAGATAGCCAGTTATCCTAATGCTCCCTTGATTTGA TGGACCACCTGGATCACACATTATGAGCCCCCTCATAAGCAGGTGGGAGTCTCAAGCGAG GGCCAGTCCCGATGGGAATAGCACTTGGTGGCTGAGGACCCTCCTATCTGTGCAGACACT GTTGTAAAACTTCACATGCATCATCTAATTTAGTCCTCACCAAAATCCTATGAAATGTAG

TCCTCACCAAAATCCTATGAAATGTAGGAATGATCATTACACCCATTTATAGATAAGGAA ACGGAGGACAGGGAGATTACTCCGCTACAGGTCAAGAGGCAGGGAAGTAGAGCTGCGAT TTGAACTGAGGTCTGTGTCTAGAACACGTGCTCATTCTTTCCCTAAAATGTATTCATAGG TGAAAAAGGGCTTCTGCGGAAAGCCCTGGGTTATGTGGGAAACCCTGGATTTACAGCTGT CTTTCCAGCAGGATGATGAGAGAGAGAGAGGGATGCGATTTCTCCCAATCTCTCCTGGTC

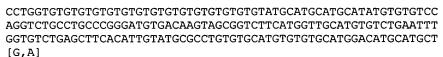
> > FIGURE 3, page 10 of 12



ACTTGTAATAGATGGTGAGTCCTCCCACAGCTGGCACCAGAGCTCCCCACTGAGGGCTGG
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GTGGTTGGATCAAGGACTCATTCCTGCCTTGGAGAAAATACTTCAACCAGAGCAGGGAGC
CTGGGGGTGTCGGGGAGGGCTGGGGATGGGGTTGGAGTATGAGGGTGGCATGCAGCT
[G, A]

AGGGCAGGGCCAGGGCTGGTGTCCCTAAGGTTGTACAGACTCTTGTGAATATTTGTATTT TCCAGATGGAATAAAAAGGCCCGTGTAATTAACCTTCACCATCAGCGCCCTAGAATCCCGG GGGGTAGGGAGTGGTATACTTTACAGGATGACAATCTTGGGAGCTAGAACTTTGTAGCC AGAGAAACTTGGGAGGTCTGGAATCTCATGTGTCTGGGGATCTTGGGGAAGAATCTTAG AAGCAGAAAACCTTGGAACATAAGAATCTTGGGGAGGGTCTAGGATCTTGAGGAGACCAG

20443 TGTTGTGAAGAGCAGCTCGCTCCTGTGCCGCCTCCTGTGCTGCCTCCATCCCTGCA GCCCAGTCGGTTCCTCTTGGCTCCTCTCGTCACTCCAGTTCCAGTCTGGCCTCTT



 $\tt GTGTGAGGCTGCAGGAAGAGGGAACAGTGGGGGATGGGCAGGAAAGTGGGCTGTGGGGTCAGGAGGGGGAT$